

<110> Farwick, Mike

Huthmacher, Klaus

Marx, Achim

Pfefferle, Walter

- <120> New Nucleotide Sequences Which Code for the menE Gene
- <130> 21123/280112
- <140> 09/834,722
- <141> 2001-04-16
- <160>
- <170> PatentIn version 3.0
- <210> 1
- <211> 1570
- <212> DNA
- <213> Corynebacterium glutamicum
- <220>
- <221> CDS
- (230)..(1357) <222>
- <400> 1 ttcgttgcca tagacatgct cttcgcagca ctgtttgcgc acgtctcctc cggcatcttt 60 120 gtcaccaaca atggttggga actcaccggc gcaatcggcg ctggcgcgct gcttctcatc gcagttggcg caggtgcatg gagcatcgac ggggttctgg caaaacgcaa ggcctaaatc 180

tagogocaca actoogaatt otgaaccato ggoactagaa totoggaat atg aat act 238

Met Asn Thr

				gca Ala												286	6
				gag Glu												334	4
				gat Asp 40												382	2
				gcc Ala												43)	0
				ggt Gly												478	8
ttg Leu	gtg Val 85	agt Ser	tcc Ser	gcc Ala	gat Asp	gct Ala 90	acg Thr	cat His	cag Gln	ttt Phe	tta Leu 95	ggt Gly	ggc Gly	gaa Glu	ggc Gly	520	6
				gcc Ala												574	4
				ctc Leu 120												62:	2
				cac His												67	0
				gac Asp												71	8
ctt Leu	aaa Lys 165	gca Ala	atg Met	gac Asp	tcc Ser	ttg Leu 170	caa Gln	ggc Gly	att Ile	gaa Glu	gcc Ala 175	ctg Leu	aaa Lys	ctt Leu	ttt Phe	76	6
gat Asp 180	gtc Val	att Ile	ctt Leu	gtt Val	ggc Gly 185	ggt Gly	gct Ala	gca Ala	ttg Leu	tct Ser 190	aag Lys	cag Gln	gcc Ala	cga Arg	att Ile 195	81	4
tct Ser	gcg Ala	gag Glu	cag Gln	cta Leu 200	gac Asp	atc Ile	aac Asn	att Ile	gtc Val 205	acc Thr	acc Thr	tac Tyr	ggc Gly	tcc Ser 210	tca Ser	86	2
gag Glu	act Thr	tca Ser	ggt Gly 215	ggc Gly	tgc Cys	gtt Val	tat Tyr	gat Asp 220	ggc Gly	aag Lys	ccc Pro	att Ile	ccc Pro 225	ggc Gly	gcg Ala	91	0

aaa gtc cgt att tcg Lys Val Arg Ile Ser 230						
gcg cag ggc tac aga Ala Gln Gly Tyr Arg 245	aat gca cct gaa Asn Ala Pro Glu 250	cat ccg gat ttc gcc His Pro Asp Phe Ala 255	aac gag 1006 Asn Glu			
ggt tgg ttt acc acc Gly Trp Phe Thr Thr 260						
acc gtg act ggt cgc Thr Val Thr Gly Arg 280	gtg gat acc gtc Val Asp Thr Val	att gat tcc ggt gga Ile Asp Ser Gly Gly 285	ttg aag 1102 Leu Lys 290			
ttg cac cca gag gta Leu His Pro Glu Val 295	ctg gaa cgt gcc Leu Glu Arg Ala 300	atc gca gat att aaa Ile Ala Asp Ile Lys 305	ggt gtc 1150 Gly Val			
acc gcg gcg tgt gtt Thr Ala Ala Cys Val 310	gtg ggt att ccc Val Gly Ile Pro 315	gat ccc cga tta ggc Asp Pro Arg Leu Gly 320	caa gca 1198 Gln Ala			
att gtg gcc gcg tac Ile Val Ala Ala Tyr 325	tcc gga tcg atc Ser Gly Ser Ile 330	agt ccg tct gaa gtt Ser Pro Ser Glu Val 335	att gaa 1246 Ile Glu			
ggc ctc gac gat cta Gly Leu Asp Asp Leu 340	cct cgt tgg cag Pro Arg Trp Gln 345	ctt ccc aaa cgg ctg Leu Pro Lys Arg Leu 350	aag cat 1294 Lys His 355			
ctg gaa tct ttg ccc Leu Glu Ser Leu Pro 360		gga aaa gct gat cga Gly Lys Ala Asp Arg 365				
atc gcg aag ctg ttt Ile Ala Lys Leu Phe 375	tagtetteat tett	gctggc tgcaactagt ttt	gccacat 1397			
cttcatcggt gtacactttg gcgatctgct catcatttcc acccatgagg gtgttgccaa 1457						
caactagtgc teceaettgg gtggtgggca egacagegaa gtgtegggge tgagegtaga 1517						
cctggcgaat agggtgatca gagcgcagtg cgcaggcatg cagccatacg tca 1570						

<210> 2

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Met Asn Thr Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro 1 5 10 15

Thr Ala Ile Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr 20 25 30

Phe Leu Pro Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg 35 40 45

Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val 50 55 60

Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr 65 70 75 80

Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly 85 90 95

Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly
100 105 110

Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala 115 120 125

Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala 130 135 140

Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro 145 150 155 160

Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu 165 170 175

Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln 180 185 190

Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr
195 200 205

Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile 210  $$\rm 215$$ 

Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly 225 230 235 240

Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe 245 250 255

Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp 260 265 270

Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly 275 280 285

Gly Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile 290 295 300

Lys Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu 305 310 315 320

Gly Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu 325 330 335

Val Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg 340 345 350

Leu Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp 355 360 365

Arg Arg Ala Ile Ala Lys Leu Phe 370 375

<210> 3

<211> 19

<212> DNA

<213> PCR primer

<400> 3 ctcactccgt tgaatttgg

- <210> 4
- <211> 19
- <212> DNA
- <213> PCR primer
- <400> 4 caggtgcatt tctgtagcc

19